Published in "Nature: 10.1038/nature10341, 2011"
which should be cited to refer to this work.

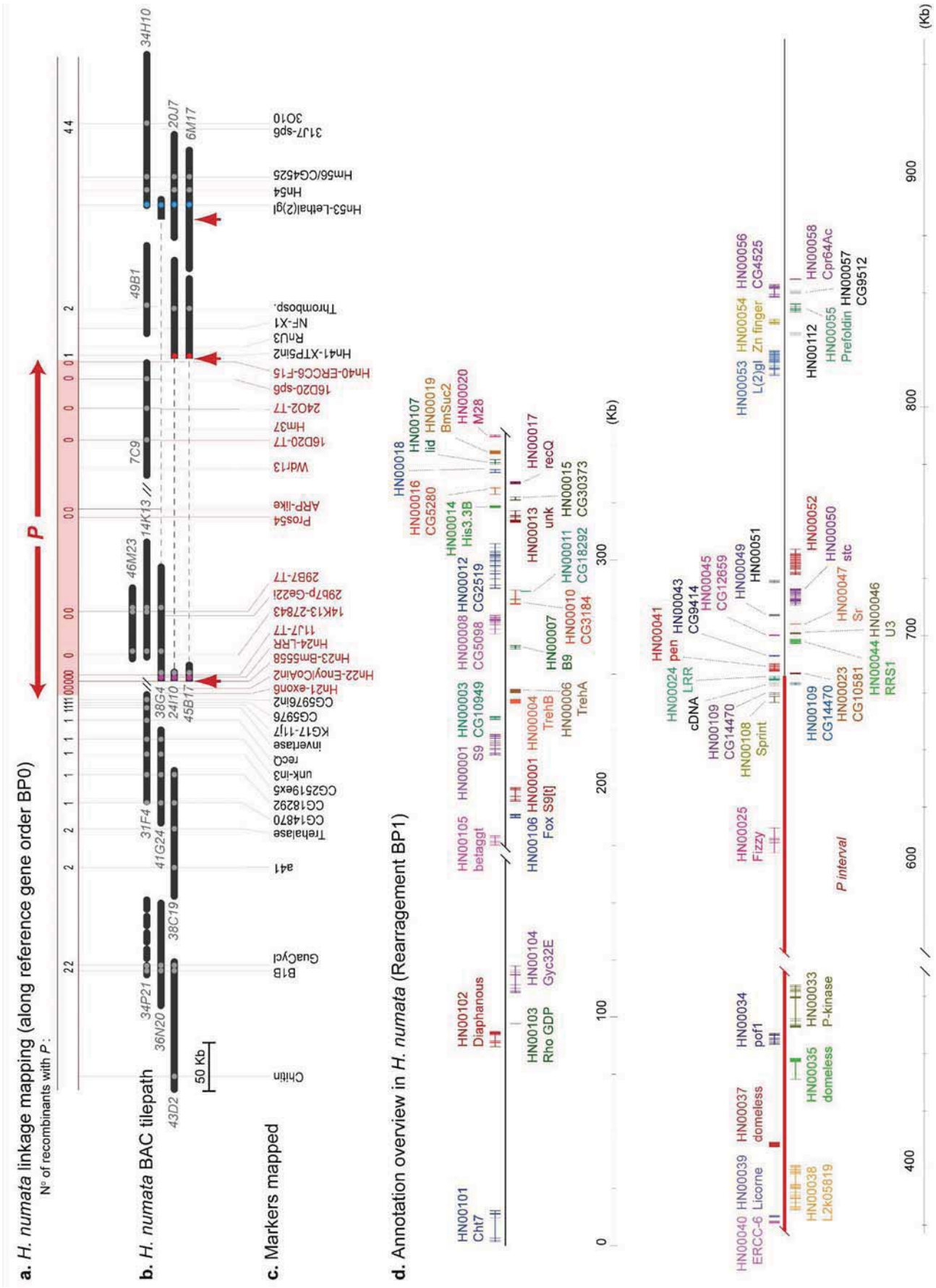


Figure S1

Figure S1. Fine mapping and annotation of the BAC tilepath,. **a.** Number of recombinants between markers and P, highlighting the 400-Kb zero-recombinant *P* mapping interval (pink block). **b**. Overlap of individual BAC clones when aligned to the *H. melpomene* reference sequence. Clones 38G4, 24I10, and 45B17 are finished and contiguous, but align to the reference sequence in two separate segments due to the rearrangements. The segments are joined on the diagram by a dotted line. Blunt ends are joined together, while round ends represent BAC ends. Red arrows indicate rearrangements breakpoints; grey dots represent shared markers used in sequencing or mapping; coloured dots represent shared markers closest to the breakpoints. **c.** Names of the markers used for mapping (see Table S6 for marker details). **d**. Graphical overview of the annotation. Exons of each putative gene are represented by separate bars of the same colour; colour coding is conserved with Fig. 2a. Also see Table S3 for gene details and orthologues

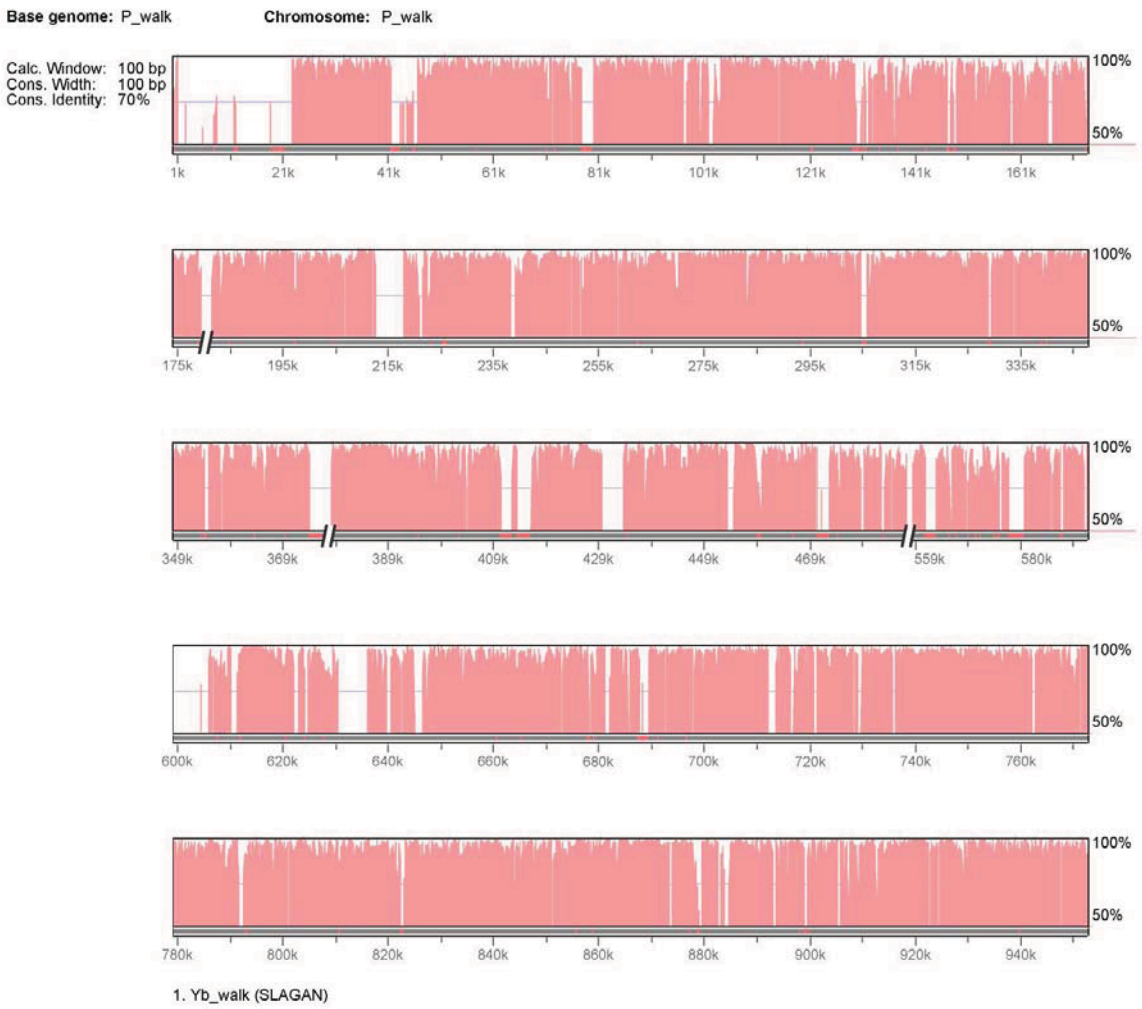


Figure S2. **Graphical overview of *H. numata* sequence similarity to *H. melpomene***. The consensus sequence for the entire *P* walk, corresponding to BP0 (reference gene order) with the different contigs concatenated, was compared to the *HmYb-HmSb* sequence using the Shuffle-LAGAN alignment program[1] and visualised using in VISTA[2,3].

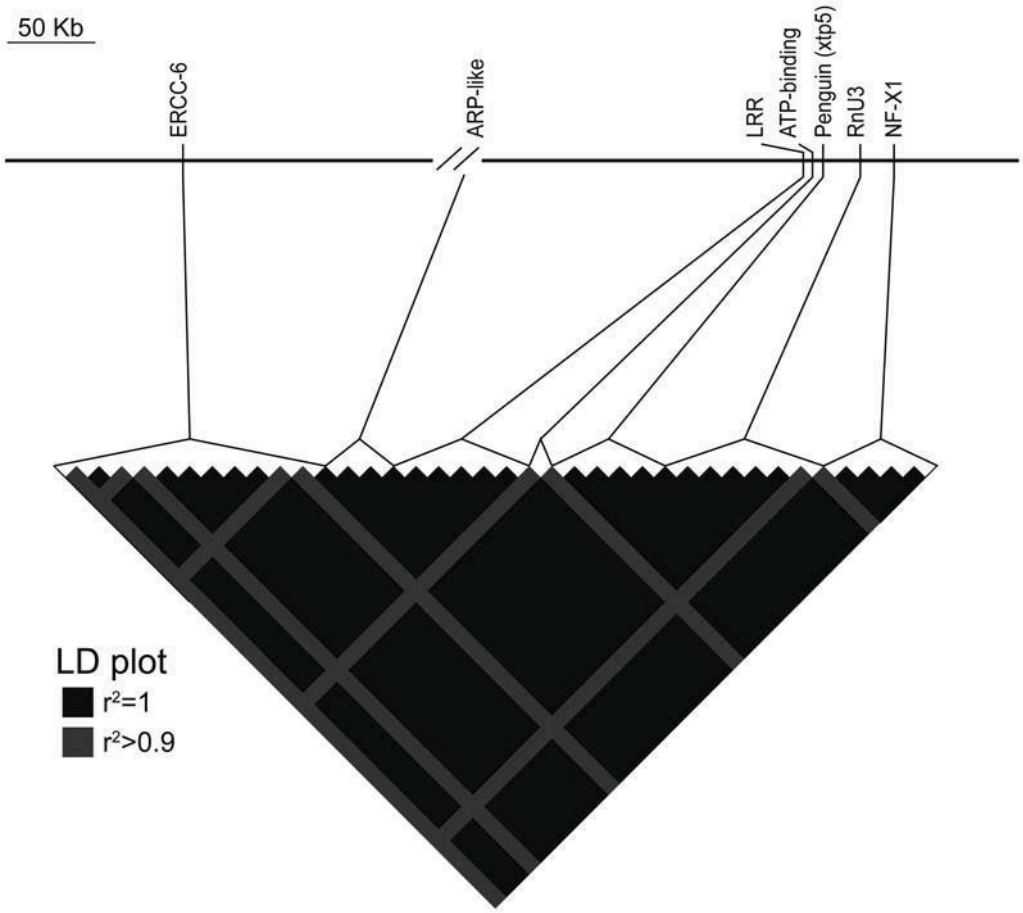


Figure S3. **Complete LD between SNPs in perfect association with pattern**. The 39 sites in our dataset whose genotypes are in complete association with colour pattern phenotypes (Fig. 2) show complete LD with each other, across a 500-kilobase segment. This segment corresponds to the position of the polymorphic rearrangements associated with mimicry polymorphism in this species, and maintaining divergent haplotypes clades causing the full LD between those associated sites. The rearrangement order shown is BP1

Figure S4.a

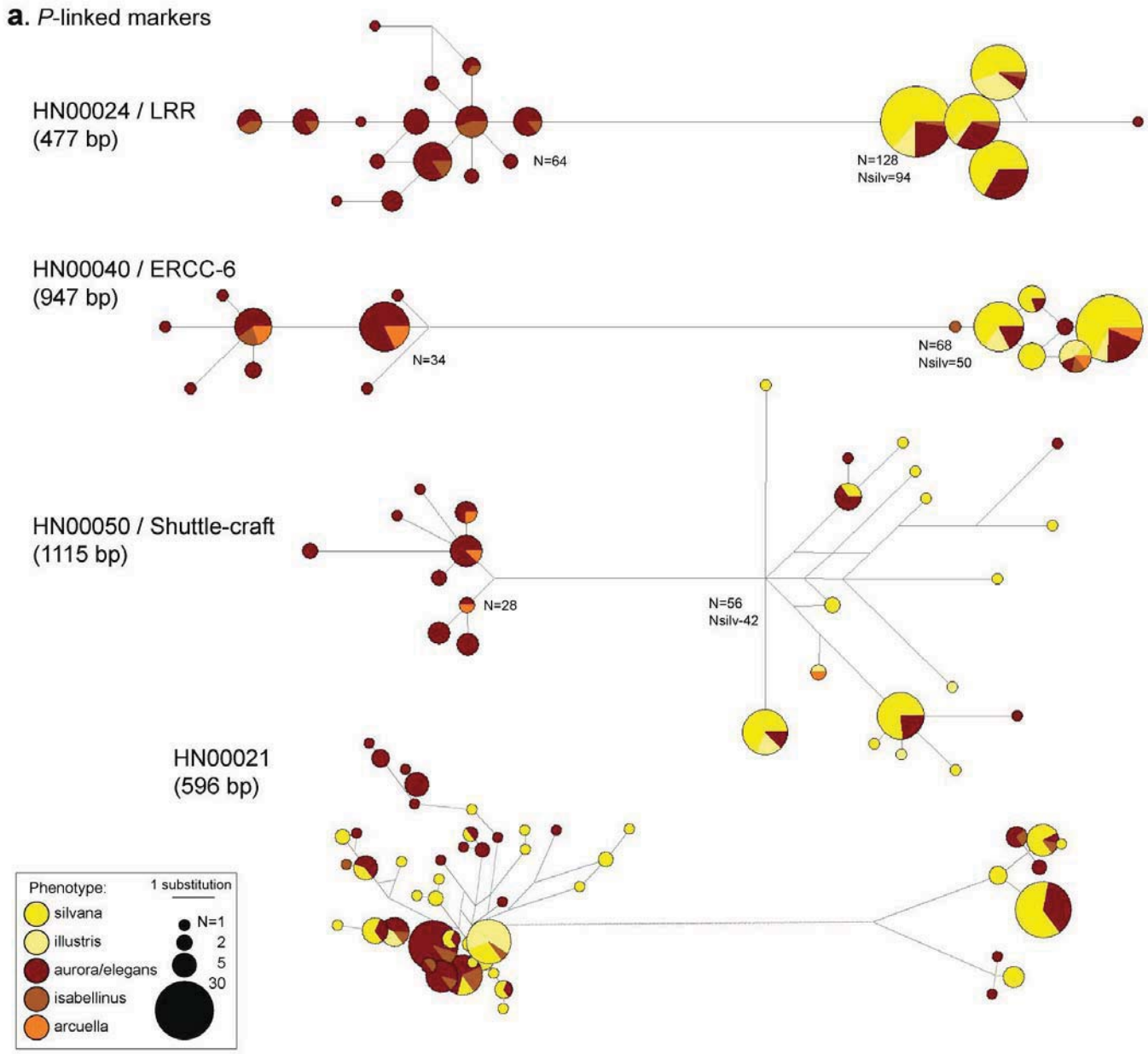
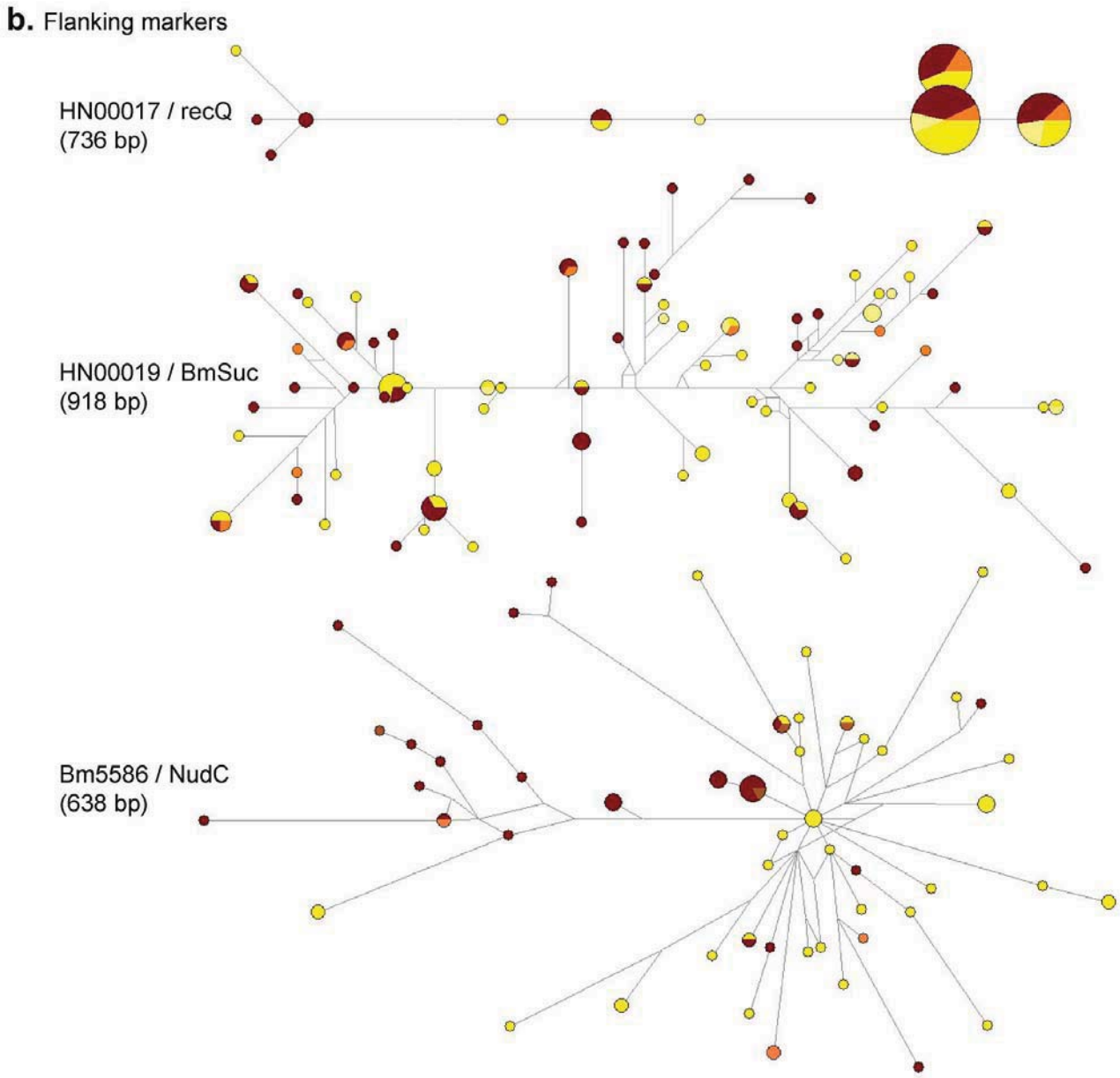


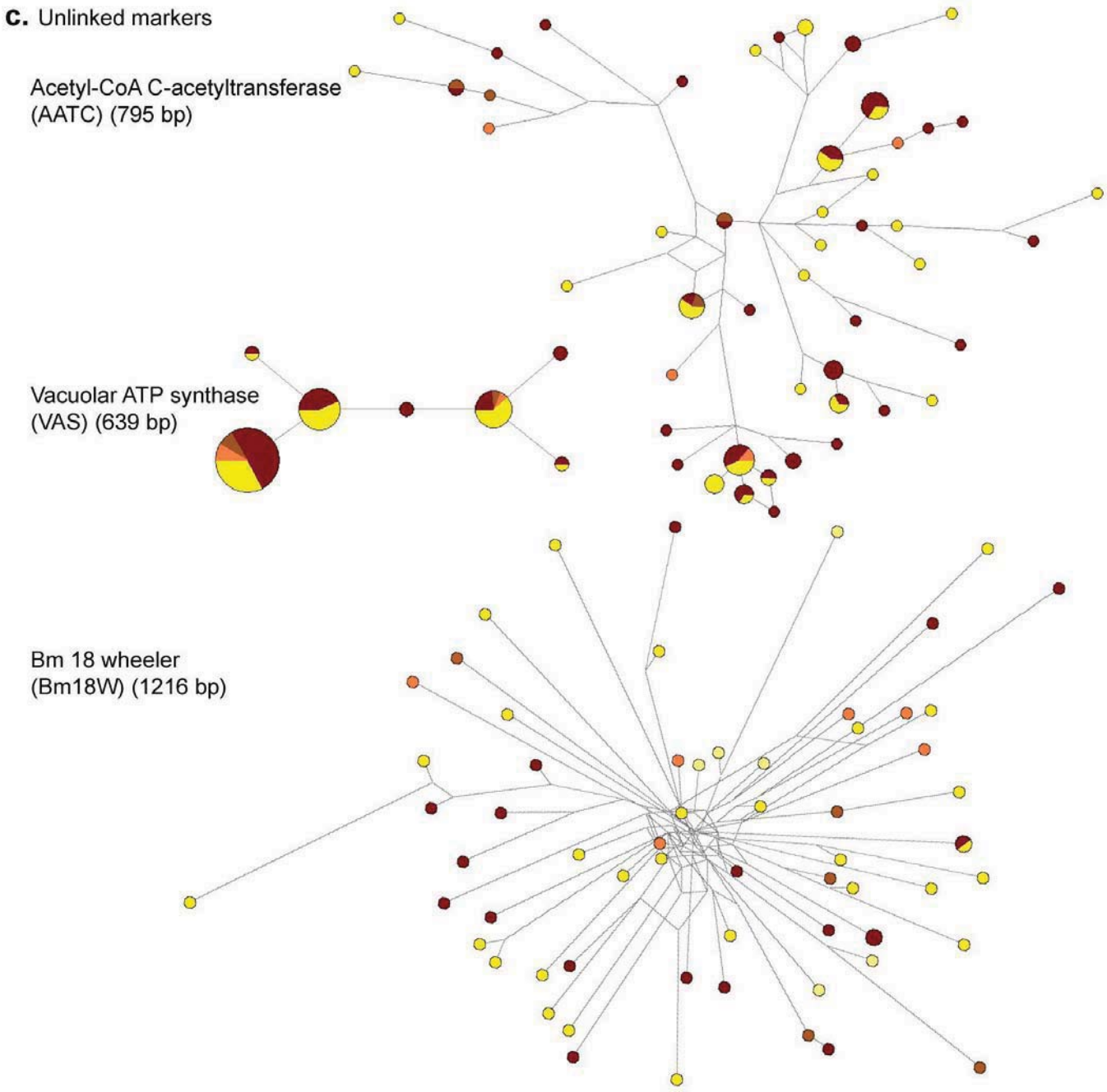
Figure S4. Comparison of haplotype networks for gene markers within and outside the supergene in Eastern Peru. Haplotype networks were constructed by parsimony using Network (see Methods). For clarity of illustration, networks shown were pre-processed by star contraction[4]. Each individual genotype is represented by its two haplotypes (see methods), coloured according to the individual's phenotype. **(a).** P-linked markers. Networks for markers within the rearrangements show a very strong haplotype structure, with a minimum of two very divergent (1-4%) haplotypes groups, indicative of suppressed recombination. Markers *ERCC-6*, *LRR* and *NF-X1*, represented here, show a perfect pattern of association with colour pattern genotype: all homozygous recessive *silvana* ($P^{sil}P^{sil}$) or *illustris* ($P^{ill}P^{ill}$) individuals, and only

Figure S4.b



these individuals, are homozygous for one haplogroup, while all *aurora* (P^{aur}-) individuals and associated phenotypes (*elegans*, *isabellinus* and *arcuella*) harbour at least one haplotype in the alternative haplogroup. This striking two-part structure remains for *HN00021*, at the boundary of the mapping interval; however, for this marker the association with colour pattern is already largely lost (Fig. 2b), as can be seen by many *silvana* individuals showing haplotypes in both haplogroups. **(b).** The networks become mostly unstructured for flanking markers on either side of the supergene (*BmSuc*, *recQ Helicase, NudC*). **(c).** Markers unlinked to *P* show a clear lack of haplotypes structuring (*Bm18W*, *VAS* and *AATC* shown –see also Table S6 and Salazar et al.[5] for marker details).

Figure S4,c



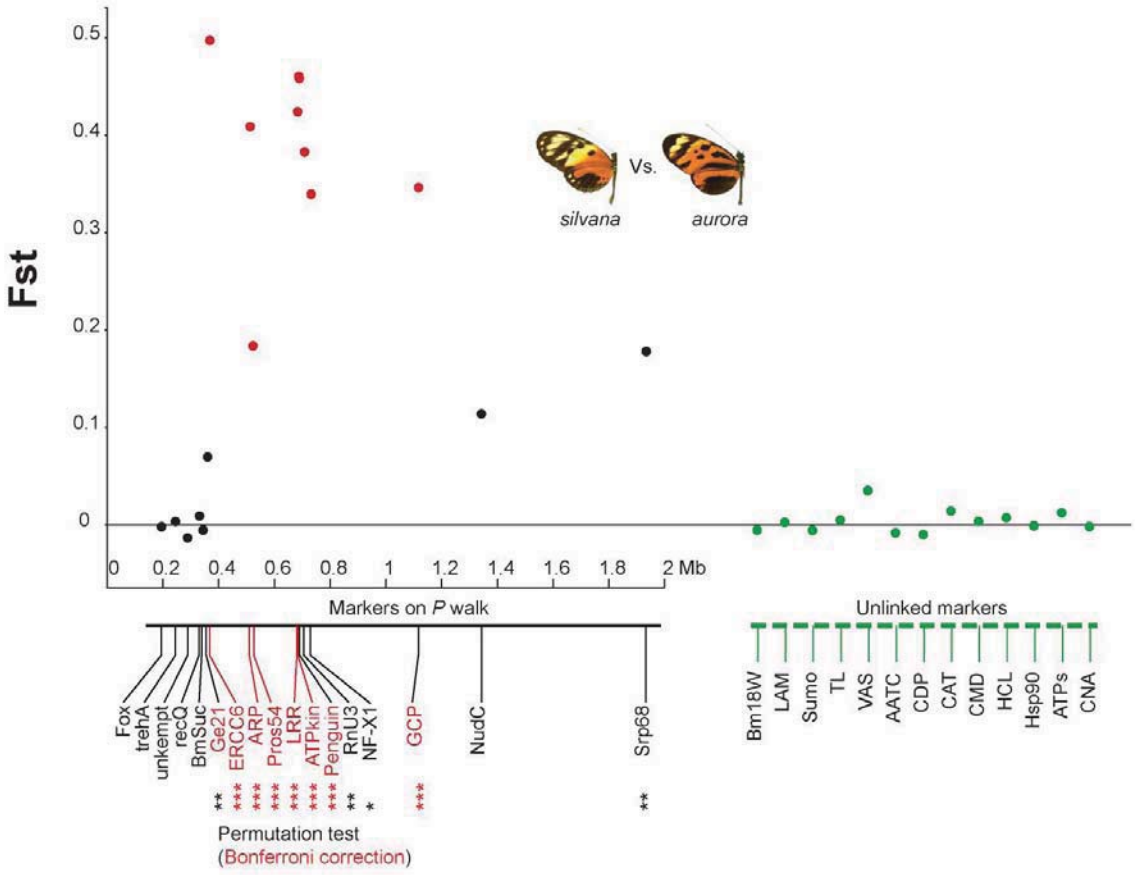


Figure S5. Fst plot of differentiation in a natural population. Fst was computed using the software DNA*sp*[7] to measure the level of genetic differentiation between individuals with the recessive *silvana* vs. *aurora* phenotype in the Yurimaguas population. Because of the allelic frequency of ~0.6 for the recessive P^{sil} allele[8], about half of *aurora* individuals are expected to be heterozygous for the recessive allele; therefore the maximum level of Fst lies around 0.5. Note that the very high level of genetic differentiation between the *aurora* and *silvana* individuals around the colour-pattern supergene *P* derives from the lack of recombination at this locus, and decays rapidly for loci outside or unlinked to the supergene.

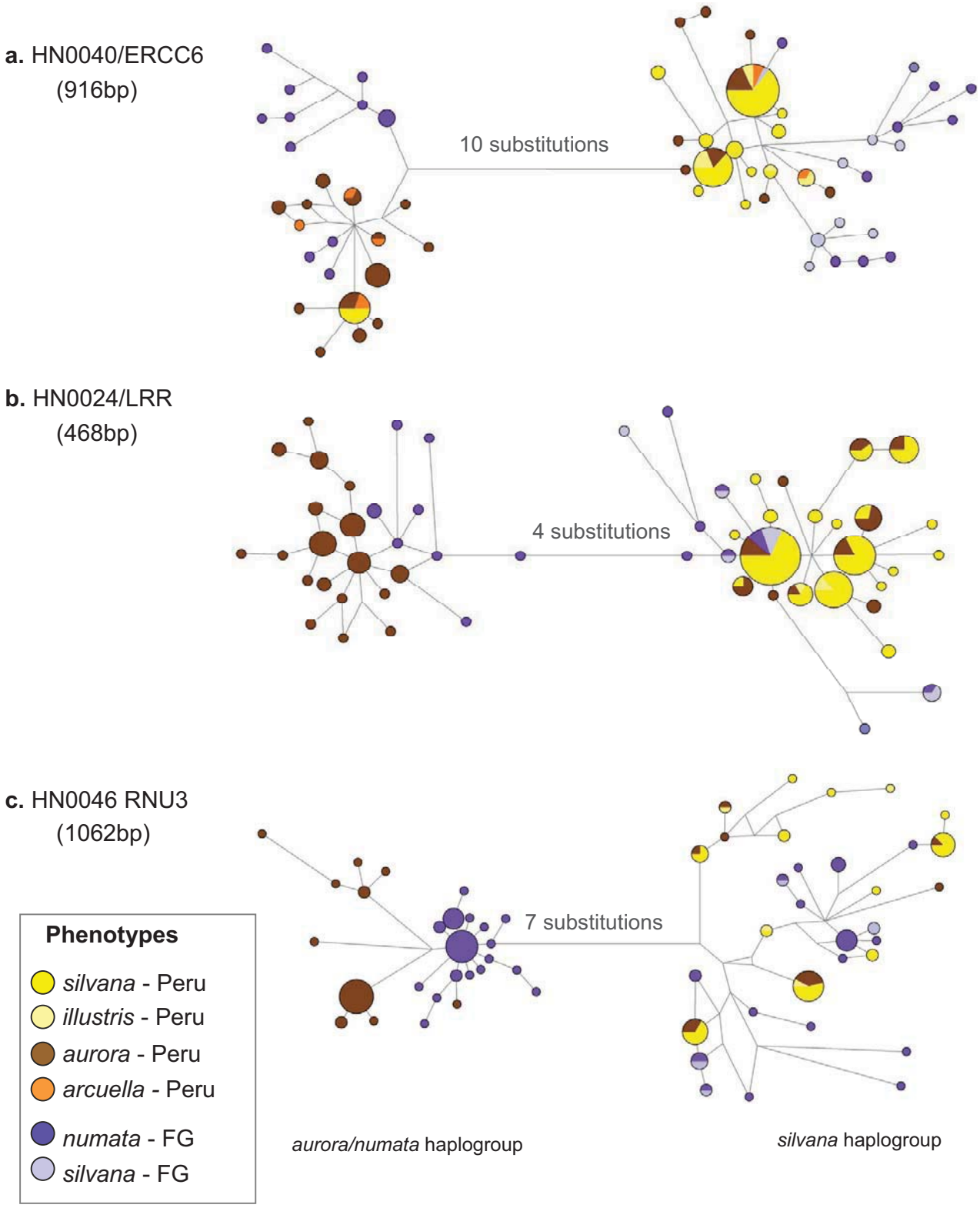


Figure S6. Conserved within-population haplotype structure between Peru and French Guiana. Haplotype networks were constructed as presented in Fig. S4 for loci within the supergene (a. ERCC6, b. LRR, c. Rnu3 –see Fig.2), including haplotypes derived from a French Guianan population. The two populations share the same *silvana* haplotype group (bottom recessive P^{sil} allele, coloured yellow for Peru and

pale blue for FG), and the dominant haplotype group containing haplotypes for similar morphs *aurora* and *numata* (P^{aur} and P^{num}, coloured brown and purple, respectively) [6]. Other colours used are orange for *arcuella*, clustering with the *aurora*/*numata* clade, except when heterozygous for a *silvana* allele. The within-population haplotypes structure as well as the perfect SNP-phenotype association, are conserved despite the 2,900 km separating Peru and French Guiana. This confirms that the network is structured primarily by phenotype across the Amazonian range, and not by population, and that the SNP-phenotype association is not a product of local population processes.

Table S1. Cross-over rate estimates in *P*-linked and unlinked regions

Brood`	Markers	LG	distance (Kb)	Total number of individuals (N)	Number of recombinants (N^{rec})	Cross-over rate (N^{rec}/nucleotide)[d]
Unlinked regions						
Brood 472	Ge03 - Ge30B	LG17	66.1	60	7	1.76×10^{-6}
Brood 472	TRP - c30739	LG13	67.8	70	5	1.05×10^{-6}
Brood 511	TRP - c30739	LG13	67.8	39	3	1.13×10^{-6}
Brood 502[a]	TRP - c6511	LG13	52.3	87	8	1.76×10^{-6}
Total unlinked regions				256	23	1.93×10^{-6}
P linked regions						
All broods[b]	B1B - Hn00021	LG15	244.5	366	2	2.23×10^{-8}
All broods[c]	Hn00021 - LRR	LG15	323.5	366	0	$<8.45 \times 10^{-9}$
All broods[b]	LRR - 3O10	LG15	321.5	366	4	3.40×10^{-8}
Total *P* and flanking regions[e]				366	6	1.78×10^{-8}

[a] An alternative marker (c6511) was used due to the absence of paternal variation at the c30739 marker
[b] Flanking regions of *P*
[c] Mapping interval for *P*
[d] calculated as the number of crossing-overs per nucleotide using the total length surveyed, in base pairs
[e] More distant loci mapping to linkage group 15 are at unknown physical distance of our *P* tilepath. Linkagemapping and recombination distances along this and other linkage groups in *H. numata* are published elsewhere[9].

Table S2. BAC clone data and accessions

Clone	Accession	Size (bp)	Overlap
6M17	FP476061	121000	24I10, 49B1, 20J7, 34H10
7C9	FP565803	115981	8K22, 38G16
14K13	CU856181	96570	46M23, 38G4
24I10	CU856182	110815	45B17, 24I10, 49B1, 6M17
31F4	CU655868	95876	41G24, 38C19
35N20	FP885880	108899	23N8
36N20	FP885855	95024	43D2, 34P21
38C19	CU914733	86858	41G24, 31F4
38G4	CU655869	140835	46M23, 14K13, 45B17, 24I10
41G24	CU914734	109797	38C19, 31F4
43D2	CU633161	131291	36N20, 34P21
45B17	CU638865	90190	38G4, 24I10, 49B1
46M23	CU856175	100298	38G4, 14K13
49A1	FP884220	91922	unlinked (on chromosome 17)
49B1	FP236755	96772	45B17, 24I10, 6M17, 20J7
34H10‡	FP885879	141031	20J7, 6M17
20J7	FP885878	108308	24I10, 49B1, 6M17, 34H10
1K7	FP885863	118130	-
8K22	FP476023	101778	8K22, 7C9
20L19	FP476047	82043	unlinked
23N8	FP885857	102695	35N20
34P21	FP885861	62129	43D2, 36N20
38G16	FP475989	78536	7C9, 38G16

‡Clones sequences below the line overlap redundantly with other clones

Table S3. Annotation of the *P* region.

Gene number	Putative gene name	Best BLASTx *D. melanogaster* hit	% identity	B. mori ortholog	% identity	Hm ortholog[$]	Hn Clone
HN00101	Cht7, chitinase-like	CG1869 / Cht7	53%	BGIBMGA005539	36%	-	43D2
HN00102	Diaphanous FH3	CG13913 / mwh	32%	BGIBMGA005540	47%	-	43D2
HN00103	Rho GDP-dissociation inhibitor	CG7823 / RhoGDI	68%	BGIBMGA005672	95%	-	43D2
HN00104	Guanylyl cyclase	CG33114 / Gyc32E	59%	BGIBMGA005671	78%	-	36N20
HN00105	Type II geranylgeranyl transferase	CG18627 / betaggt	50%	BGIBMGA005544	69%	-	41G24
HN00106	Fork head transcription factor	CG11799 / mnf	39%	BGIBMGA005669	60%	-	41G24
HN00001	Peptidase S9 (truncated?)	no hit	-	BGIBMGA005667	41%	HM00001	41G24
HN00002	Peptidase S9	no hit	-	BGIBMGA005667	47%	HM00002	41G24
HN00003	CG10949	CG10949	31%	BGIBMGA005547	69%	HM00003	41G24
HN00004	Trehalase	CG9364 / Treh	32%	BGIBMGA005665	69%	HM00004 [HmYb]	41G24
HN00006	Trehalase	CG9364 / Treh	41%	BGIBMGA005664	60%	HM00006 [HmYb]	41G24
HN00007	B9 protein	CG14870	33%	BGIBMGA005663	59%	HM00007 [HmYb]	41G24
HN00008	CG5098	CG5098	75%	BGIBMGA005548	65%	HM00008 [HmYb]	41G24
HN00010	CG3184	CG3184	38%	BGIBMGA005662	56%	HM00010 [HmYb]	41G24
HN00011	CG18292	CG18292	83%	BGIBMGA005661	82%	HM00011 [HmYb]	41G24
HN00012	CG2519	CG2519	45%	BGIBMGA005549	47%	HM00012 [HmYb]	31F4
HN00013	unkempt	CG4620 / unk	86%	BGIBMGA005660	70%	HM00013 [HmYb]	31F4
HN00014	Histone H3	CG8989 / His3.3B	100%	BGIBMGA005550	100%	HM00014 [HmYb]	31F4
HN00015	CG30373	CG30373	46%	BGIBMGA005659	55%	HM00015 [HmYb]	31F4
HN00016	CG5280	CG5280	50%	BGIBMGA005551	59%	HM00016 [HmYb]	31F4
HN00017	RecQ Helicase	CG6920 / mus309	40%	BGIBMGA005666	61%	HM00017 [HmYb]	31F4
HN00018	Phox-like	no hit	-	BGIBMGA005553	71%	HM00018 [HmYb]	31F4
HN00107	little imaginal discs	CG9088 / lid	46%	BGIBMGA005554	31%	-	31F4
HN00019	BmSuc2 beta-fructofuranosidase	no hit	-	BGIBMGA005555	55%	HM00019 [HmYb]	31F4
HN00020	Peptidase M28	CG5976	55%	BGIBMGA005556	70%	HM00020 [HmYb]	31F4
HN00040*	ERCC-6	CG4261 / Hel89B	34%	BGIBMGA005640	63%	HM00040	7C9
HN00039*	Licorne MAP kinase	CG12244 / licorne	67%	BGIBMGA005641	89%	HM00039	7C9
HN00038*	lethal (2) k05819	CG3054 / lethal (2) k05819	45%	BGIBMGA005562	61%	HM00038	7C9
HN00037*	domeless, tyrosine phosphatase	CG14226 / dome	25%	BGIBMGA005642	56%	HM00037	7C9
HN00036*	washout	CG13176 / wash	27%	BGIBMGA005643	65%	HM00036	7C9

HN00035*	domeless, tyrosine phosphatase	CG14226 / dome	29%	BGIBMGA005642	56%	HM00035	7C9
HN00034*	F-box/WD-repeat protein pof1	no hit	-	BGIBMGA005645	51%	HM00034	7C9
HN00033*	Protein-kinase-like	CG32580 / mucin 14A	20%	BGIBMGA005561	44%	HM00033 [HmSb]	7C9
HN00028*†	Putative Manf	CG7013 / Manf	80%	BGIBMGA005559	79%	HM00028 [HmSb]	gap
HN00030*†	Proteasome 54kD subunit	CG7619 / Pros54	61%	BGIBMGA005560	79%	HM00030 [HmSb]	gap
HN00025*	Fizzy	CG4274 / Fzy	25%	BGIBMGA005652	52%	HM00025 [HmYb]	38G4
HN00108*	Sprint	CG34414 / Spri	40%	BGIBMGA005653	85%	-	38G4
HN00109*	CG14470	CG14470	26%	BGIBMGA005654	68%	-	38G4
HN00110*	HN00110	no hit	-	BGIBMGA005558	69%	-	38G4
HN00024*	LRR	CG5407 / Sur-8	25%	BGIBMGA005655	39%	HM00024 [HmYb]	38G4
HN00023*	HN00023	CG10581	42%	BGIBMGA005557	52%	HM00023 [HmYb]	38G4
HN00041*	penguin	CG1685 / pen	35%	BGIBMGA005638	62%	HM00041	24I10
HN00042*	Thymidylate kinase	CG5757	34%	no hit	-	HM00042	24I10
HN00043*	CG9414	CG9414 / Drep-4	34%	BGIBMGA005639	75%	HM00043	24I10
HN00044*	RRS1	CG32409	55%	BGIBMGA005564	67%	HM00044	24I10
HN00045*	CG12659	CG12659	55%	BGIBMGA005565	81%	HM00045	24I10
HN00046*	U3 snoRNA	CG33505 / U3-55K	50%	BGIBMGA005636	78%	HM00046	24I10
HN00047*	Sr protein	CG5442 / SC35	83%	BGIBMGA005635	86%	HM00047	24I10
HN00049*	HN00049	CG15040	18%	BGIBMGA005566	33%	HM00049	24I10
HN00050*	Shuttle-craft	CG3647 / stc	36%	BGIBMGA005634	46%	HM00050	24I10
HN00051*	HN00051	CG6793	22%	BGIBMGA005567	64%	HM00051	24I10
HN00052*	Thrombospondin	no hit	-	BGIBMGA005633	52%	HM00052	24I10
HN00053*	lethal (2) giant larvae	CG2671 / l(2)gl	44%	BGIBMGA005570	83%	HM00053	6M17, 38G4
HN00112	HN00112	no hit	-	BGIBMGA008616	50%		6M17
HN00054	Zn finger protein	CG10366	28%	BGIBMGA005571	40%	HM00054	6M17
HN00055	Prefoldin	CG41265	27%	BGIBMGA005632	66%	HM00055	6M17
HN00056	Tetratricopeptide repeat protein	CG4525	51%	BGIBMGA005572	69%	HM00056	6M17
HN00057	Putative Ecdysone oxidase	CG9512	33%	BGIBMGA005711	41%	HM00057	6M17
HN00058	cuticular protein RR-2 motif 74	CG15008 / Cpr64Ac	68%	BGIBMGA005631	83%	HM00058	6M17
HN00059	CG6734	CG6734 /	43%	BGIBMGA005629	59%	HM00059	34H10
HN00060	rudimentary-like	CG3593 / rudimentary-like	51%	BGIBMGA005628	71%	HM00060	34H10
HN00061	Kruppel homolog	CG7368 / Lethal (3) neo38	41%	BGIBMGA005626	52%	HM00061	34H10
HN00113	Kruppel homolog	CG14938 / crol	28%	BGIBMGA005575	76%	-	34H10
HN00114	Kruppel homolog	CG7368	82%	BGIBMGA005627	96%	-	34H10
HN00115	globin 1	no hit	-	BGIBMGA005612	63%	-	35N20

HN00116	gawky	CG31992 / gw	44%	BGIBMGA005589	73%	-	35N20
HN00117	CG5262	CG5262	53%	BGIBMGA005613	73%	-	35N20
HN00118	CG10254	CG10254	55%	BGIBMGA005588	81%	-	35N20
HN00119	RabGAP Regulator	CG5337	58%	BGIBMGA005614	83%	-	35N20
HN00120	Alcohol dehydrogenase	CG17221	28%	BGIBMGA005615	67%	-	35N20
HN00121	putative NudC	CG31251	32%	BGIBMGA005586	61%	-	35N20
HN00122	CG6398	CG6398	46%	BGIBMGA005617		-	35N20

* Gene in a rearranged chromosomal segment

$ Superscripts indicate genes in *HmYb* or *HmSb* interval in *H. melpomene*

Table S4. Sequence similarity to *H. melpomene HmYb-HmSb* region

Clone[†]	Conserved	Conserved length (bp)
6M17	84%	101605
7C9	75%	87429
14K13	69%	66528
20J7	84%	46930
24I10[‡]	88%	89057
31F4	87%	83666
34H10	84%	118293
36N20	79%	74983
38C19	84%	73050
38G4[‡]	50%	65467
41G24	85%	93781
43D2	80%	87688
49B1	81%	27499
Consensus P walk	**75%**	**649756**

[†] Redundant clones omitted

[‡] Clone with a rearrangement breakpoint: calculation based on longer side of breakpoint. Note that the longer side of breakpoint BP1 is shorter in clone 45B17 than in 24I10, so the latter is shown.

Table S5. List of specimens from natural populations

Code	H. numata form	Sex	Location	Latitude	Longitude	Country
b001-MJ05	*bicoloratus*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b004-MJ05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b005-MJ05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b007-MJ05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b011-MJ05	*bicoloratus*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b012-MJ05	*bicoloratus*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b122-MJ05	*bicoloratus*	male	Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
t003-m05	*tarapotensis*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t008-m05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t036-m05	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t057-m05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t058-m05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t060-m05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t063-m05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t1328-05	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
o1273_05	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o1275_05	*aurora*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o140_m05	*aurora (x arcuella)*	female	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o207_m05	*aurora*	female	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
e1277_05	*aurora (var. elegans)*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
e139_m05	*aurora (var. elegans)*	female	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
L1266_05	*aurora (var. isabellinus)*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
L1270_05	*aurora (var. isabellinus)*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s089_m99	*silvana*	male	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
s093_m99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s094_m99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s095_m99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s096_m99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s097_m99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s224_m02	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s225_m02	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru

Additional specimens for Association and LD studies (fig. 2)

a044_m99	*arcuella*	male	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
a077_m99	*arcuella*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
a1274_05	*arcuella*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
a202_m05	*arcuella*	male	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o076_m99	*aurora*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o1206_05	*aurora*	female	km 6 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o1207_05	*aurora*	female	km 6 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o1244_05	*aurora*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o1264_05	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o1269_05	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o1272_05	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o129_m02	*aurora*	female	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o132_m99	*aurora*	female	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o149_m99	*aurora*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o203_m05	*aurora*	male	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o206_m05	*aurora*	male	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o215_m02	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o253_M02	*aurora*	male	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o256_m02	*aurora*	female	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o293_m02	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o294_m02	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o1265_05	*aurora*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o1267_05	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o208_m05	*aurora*	female	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
o1268_05	*aurora (var.)*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
g078_m99	*aurora (var. isabellinus)*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s124_m05	*silvana*	male	Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
s1240_05	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s1241_05	*silvana*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s1242_05	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s1271_05	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s1278_05	*silvana*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
s129_m05	*silvana*	male	Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
s130_m02	*silvana*	female	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru

s132_M02	*silvana*	female	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
s183_m05	*silvana*	male	Alianza km 80 Tarapoto-Yurimaguas	6°7'54.51"S	76°16'7.33"W	Peru
s184_m05	*silvana*	male	Alianza km 80 Tarapoto-Yurimaguas	6°7'54.51"S	76°16'7.33"W	Peru
s205_m05	*silvana*	male	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
s219_m02	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s221_M02	*silvana*	female	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s247_M02	*silvana*	male	km 7.5 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
s472_m02	*silvana*	female	Ex larva Pintoyaquillo 5 km NW Convento	6°15'05.04"S	76°18'48.96"W	Peru
s547_m02	*silvana*	male	Villa Autonoma, Tarapoto	6°28'43.07"S	76°21'18.60"W	Peru
Additional specimens for Haplotype networks and Short-fragment Breakpoint assays (fig. S4, S5)						
a1243-05	*arcuella*	female	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o100_M99	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o102_M99	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o104_M99	*aurora*	female	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o105_M99	*aurora*	female	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o228_M02	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o229_M02	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o043_M99	*aurora*	female	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o064_M99	*aurora*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o075_M99	*aurora*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o079_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o080_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o081_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o082_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o084_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o085_M99	*aurora*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
o090_M99	*aurora*	male	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
o098_M99	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o099_M99	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o217-m02	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
o227-m02	*aurora*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
o106-m99	*aurora*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
e421_M02	*aurora (var. elegans)*	male	Ex larva km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
e425_M02	*aurora (var. elegans)*	male	Ex larva km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
g103_M99	*aurora (var. isabellinus)*	female	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru

g106_M99	*aurora (var. isabellinus)*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
g083_M99	*aurora (var. isabellinus)*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s168_M97	*silvana*	male	Túnel km 20 Tarapoto-Yurimaguas	6°27'2.67"S	76°17'26.47"W	Peru
s178_M99	*silvana*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
s067_M99	*silvana*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s068_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s069_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s070_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s071_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s072_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s073_M99	*silvana*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
s087_M99	*silvana*	male	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
s088_M99	*silvana*	male	km 7.2 Pongo-Barranquita	6°17'22.02"S	76°13'43.74"W	Peru
s091_M02	*silvana*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
s092_M99	*silvana*	male	Pongo de Cainarachi km 60 TY	6°20'30.11"S	76°17'52.98"W	Peru
s155-m99	*silvana*	male	km 10 Tarapoto-Yurimaguas	6°27'43.00"S	76°19'23.00"W	Peru
s64b-m99	*silvana*	female	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'55.00"S	76°15'50.00"W	Peru
i086_M99	*illustris*	male	Davidcillo km 72 Tarapoto-Yurimaguas	6°14'24.50"S	76°16'12.84"W	Peru
i204_M05	*illustris*	male	km 6.5 Pongo-Barranquita	6°17'51.12"S	76°14'3.96"W	Peru
i1189_05	*illustris*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
i121_M05	*illustris*	female	Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
i1276_05	*illustris*	male	km 26 Yurimaguas-Tarapoto	5°58'29.34"S	76°13'51.36"W	Peru
i153_M97	*illustris*	male	km 10 Tarapoto-Yurimaguas	6°27'43.00"S	76°19'23.00"W	Peru
i155_M97	*illustris*	male	km 10 Tarapoto-Yurimaguas	6°27'43.00"S	76°19'23.00"W	Peru
i161_M02	*illustris*	female	La Antena km 17 Tarapoto-Yurimaguas	6°27'10.08"S	76°17'55.32"W	Peru
i166_M97	*illustris*	male	Túnel km 20 Tarapoto-Yurimaguas	6°27'2.67"S	76°17'26.47"W	Peru
i1359-05	*illustris*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b006-MJ05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b028-MJ05	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b29-m05	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b30-m05	*bicoloratus*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b34-m05	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b35-m05	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b54-m05	*bicoloratus*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b59-m05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru

b61-m05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b62-m05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b123-m05	*bicoloratus*		Fundo Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
b125-m05	*bicoloratus*		Fundo Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
b126-m05	*bicoloratus*		Fundo Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
b127-m05	*bicoloratus*		Fundo Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
b64-m05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b79-m05	*bicoloratus*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b86-m05	*bicoloratus*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
b140-m02	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b150-m02	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b212-m02	*bicoloratus*	male	km 10-12 Tarapoto-Yurimaguas	6°27'43.00"S	76°19'23.00"W	Peru
b263-m02	*bicoloratus*	female	Puente Rio Serranoyacu Rioja	5°40'28.85"S	77°40'10.88"W	Peru
b267-m02	*bicoloratus*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b282-m02	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b283-m02	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
b731-m02	*bicoloratus*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
ba73-m97	*bicoloratus*	male	Cataratas del Ahuashiyacu km14 TY	6°27'15.60"S	76°18'24.99"W	Peru
t1187-05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t1188-05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t1191-05	*tarapotensis*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t1327-05	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t1358-05	*tarapotensis*	female	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
t1360-05	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t1361-05	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t1362-05	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t1363-05	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t1365-05	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t50-m97	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t53-m97	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t56-m97	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t69-m97	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t71-m97	*tarapotensis*	female	Cataratas del Ahuashiyacu km14 TY	6°27'15.60"S	76°18'24.99"W	Peru
t146-m02	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t163-m02	*tarapotensis*	male	La Antena km 17 Tarapoto-Yurimaguas	6°27'10.08"S	76°17'55.32"W	Peru

t176-m02	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t203-m02	*tarapotensis*	female	Shapaja Quebrada Pucayaquillo	6°35'10.00"S	76°13'5.00"W	Peru
t206-m02	*tarapotensis*	female	Chumía, Chazuta	6°37'1.77"S	76°11'4.55"W	Peru
t207-m02	*tarapotensis*	female	Chumía, Chazuta	6°37'1.77"S	76°11'4.55"W	Peru
t211-m02	*tarapotensis*	male	km 10-12 Tarapoto-Yurimaguas	6°27'43.00"S	76°19'23.00"W	Peru
t268-m02	*tarapotensis*	female	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t270-m02	*tarapotensis*	male	Fundo Biodiversidad km19 Tarapoto-Yurimaguas	6°27'40.47"S	76°17'7.04"W	Peru
t272-m02	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
t284-m02	*tarapotensis*	male	Rio Shilcayo, Tarapoto	6°27'20.00"S	76°20'40.00"W	Peru
a1192-05	*arcuella*	male	Urahuasha km 8 Tarapoto-Yurimaguas	6°27'50.11"S	76°19'51.30"W	Peru
u131-m99	*arcuella (var. lutea)*	male	Shapaja Quebrada Pucayaquillo	6°35'10.00"S	76°13'5.00"W	Peru
n4123-M09	*numata*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4124-M09	*numata*	female	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4183-M09	*numata*	female	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4111-M09	*numata*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4112-M09	*numata*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4125-M09	*numata*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4181-M09	*numata*	female	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4182-M09	*numata*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4196-M09	*numata*	female	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
n4146-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4147-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4143-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4144-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4145-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4148-M09	*numata*	male	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4149-M09	*numata*	male	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4150-M09	*numata*	male	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4152-M09	*numata*	male	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4153-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4154-M09	*numata*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
n4023-M09	*numata*	male	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4024-M09	*numata*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4242-M09	*numata*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4020-M09	*numata*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG

n4021-M09	*numata*	male	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4022-M09	*numata*	male	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4051-M09	*numata*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4053-M09	*numata*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4054-M09	*numata*	male	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
n4225-M09	*numata*	female	Route de Cacao, Montagne Grosse Roche	4°33'52.14"	52°25'36.74"	FG
n4226-M09	*numata*	female	Route de Cacao, Montagne Grosse Roche	4°33'52.14"	52°25'36.74"	FG
n4223-M09	*numata*	female	Route de Cacao, Montagne Grosse Roche	4°33'52.14"	52°25'36.74"	FG
n4224-M09	*numata*	female	Route de Cacao, Montagne Grosse Roche	4°33'52.14"	52°25'36.74"	FG
n4241-M09	*numata*	female	Route de Kaw, Escol+2km			FG
n4017-M09	*numata*	female	Route de Regina, Morne aux Echos	4°38'9.45"	52°21'38.52"	FG
s4122-M09	*silvana*	female	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
s4184-M09	*silvana*	male	Les Nouragues Inselberg	4°5'0.10"	52°40'31.46"	FG
s4151-M09	*silvana*	female	Les Nouragues-Saut Pararé	4°1'50.75"	52°40'57.31"	FG
s4025-M09	*silvana*	female	Patawa Laie#3	4°33'43.91"	52° 9'24.99"	FG
s4010-M09	*silvana*	female	Route de Regina, Morne aux Echos	4°38'9.45"	52°21'38.52"	FG

Table S6. Short-range PCR breakpoint assay.

			Positive assays		
Population	**Morph**	***N***	**BP1**	**BP2**	**BP0**
Yurimaguas, Peru	*silvana*	34			**34** (100%)
(n=82)	*aurora*	42		**42** (100%)[a]	28
	arcuella	6		**6** (100%)	4
Tarapoto, Peru	*illustris*	8			**8** (100%)
(n=74)	*tarapotensis*	34		**34** (100%)	12
	bicoloratus	32	**30** (94%)	17	9
French Guiana	*silvana*	5			**5** (100%)
(n=40)	*numata*	35		**35** (100%)	28

[a] Percentages indicate the proportion of positive assays for the breakpoint associated with the expressed phenotype.

Table S7. Breakpoint primer pairs

Breakpoint	Clone	Expected product size (bp)	Gene name	Primer Sequence
BP0-Long range	bHN7C9	5609	HN00040	TTGCAATTTTAATCGCTTCC
	bHN45B17		HN00041	GTTAGTGCCCTGCCAAACAC
BP0-short range	bHN7C9	1100-1300[a]	HN00040	TGCAATAGCCAATTGAGTCT
	bHN45B17		HN00041	TCAAATACTTCCRCAGTAGC
BP1-Long range	bHN45B17	2592	HN00041	GTTAGTGCCCTGCCAAACAC
	bHN38G4		HN00023	CCATTTTGCCAATTTCGTCT
BP1-short range	bHN24I10	457	na	GCAAAATCCCTTGAGAGCTG
	bHN24I10		na	TTCCCGCATTTTATTTCGTC
BP2-Long range	bHN6M17, 38G4	2432	HN00053	CCTATCGACGCATTTTATTC
	bHN38G4		HN00023	CCATTTTGCCAATTTCGTCT
BP2-short range	bHN38G4	324	na	GCGGCTAGCACTTAAACAGC
	bHN38G4		na	TCGGTCTCGGTCAAAAAGTC

[a] polymorphic fragment length

Table S8. Marker and primer details

Marker name	Clone	Estimated walk position (Kb)[†]	Length (bp)	Gene name[‡]	Forward primer	Reverse primer
P-linked markers						
B1B	43D2	115929	514	intergenic	GTAGGGATTTTAGGTTATGGTTTT	AACATATTATCGGCTTCGTCA
GuaCycl	43D2	121879	655	HN00104	GCGACGCCATCATATCCTAT	CGTATATTGGGCACGGAATC
Fox	41G24	195995	681	HN00106	CTGCAGATTGGGCTGATTTT	CATTCGATTTCAACGGTGTG
a41	41G24	201268	357	intergenic	ATCGTCGAACTCCTGACCAC	TTTTGTTCCACTATTACGCAAAAA
B1A	41G24	206838	410	intergenic	CTACTACTGCGCTACAAAGGTC	TGAGTAGAGATGCCAAAAAGTA
Trehalase1A	41G24	246620	710	HN00006	AGCCCTGAACGTAAGCAAGA	ACATGAGCACCCTCAACTCC
CG14870	41G24	266045	772	HN00007	TGCGAGAATCTGGAGTAACAAA	GGTCTACCAGCTCTGGATGC
CG18292	41G24	289368	251	HN00011	TCAGTGATATGGAAGCGATGGAT	AATGCCTCTTTTTAGTCTTTCTGC
CG2519in5	31F4	302294	661	HN00012	TTACTGGTGTTCCCGTTGGT	GTGACGCAGAGGCACAGTTA
unk-in1	31F4	320341	622	HN00013	TCCAGATGGAACTGATGGTG	GGCAGGCATACCCTTGTCTA
recQ	31F4	333478	736	HN00017	CGGGCAGCATTCTCAATTAT	TGTTCTCAGTGGGGACATGA
invertase/BmSuc	31F4	346506	918	HN00019	AATTGGGGACACGCTGTAAG	AATACGCACGCCTAATACCG
KG17-11j7	31F4	351529	187	HN00020	CAACATTAAGAATGGGGTAGGAG	TGCTTACCTTTTCTTGATAGAATTT
CG5976	31F4	353577	721	HN00020	TAAATCCCGATGCCGATAGA	CACCGCCGAGTCTGTAGC
CG5976in2	31F4	353577	921	HN00020	CACATCAAACGCCGTAATTG	AGTTGTCACGAGACGTGTGC
Hm21ex6	gap	360475	601	HN00021	AAAAATCAAGGAAGAATAAAGATGC	TCCAGCAAAGATCCTTTGAAC
EnoyalCoAin2	gap	365475	832	HN00022	TCAGGAGGCTGAGAAGATGG	GAAGACGCGGCTTACAAGA
ERCC6-F15	7C9	370545	947	HN00040	ATCACATGGCGGAAATCATC	GCTGACCAATTCTCCATGCT
16D20-sp6	7C9	395721	519	intergenic	GTTCGGCACACCATATCCTC	GAGTTCAATCCGCCATTTGT
30F8-sp6	7C9	442278	529	HN00035	TTGCTGTGTATCCACTTGGTG	ATATCTCGGTTGGCTGCTTG
Wdr13	7C9	451148	250	HN00034	CTCCTGAGTTCGGTGGAAAG	CCAGTAACCGGTTCGCTATG
16D20-T7	7C9	470956	851	intergenic	ATCTGATGCGAAGGAAGTGG	GGGATGTCGACGCTAGAAAA
Pros54	gap	521456	756	Hm00030	CAACAAGACTGCAGGCACAG	TTCAGCCTGTGGAGCTTCTT
ARP-like	gap	526456	434	Hm00028	TGGTGTGTTTTATTTATTATTCCTGGT	TCAGATCTACCCATATATCTAGGTTTT
29b7-T7	14K13	573381	410	intergenic	TTCAATGGCAAGCTTAGTATGTCA	AATTAGTGTGGTGTGGTGCCTTAT
14k13B	14K13	584709	708	intergenic	AGGCAGAGGAAACGGTGTTA	CTCAAAGGTGGGGAAAAACA
LRR	38G4	683935	477	HN00024	TGGAGGAAAATGAAAACAAACC	GATGTCCCCAAACAAATGGA

ATP-Bm5558	38G4	687036	244	HN00023	AGGCTTTTGACCGAGGAAGT	CCATTTTGCCAATTTCGTCT
XTP5in2	45B17	693662	364	HN00041	GTTAGTGCCCTGCCAAACAC	TGCAAGGAATTGCACATTTT
RnU3	45B17	712951	1062	HN00046	CGCTCCTAACCTCGAAAATG	GTGCTCCTGCCCTATAGCTG
NF-X1	45B17	736354	1136	HN00050	CCTCCTAATAATTGGAATGGTGA	CCACAGACGATTTATGTCTTCC
Thrombosp.	45B17	754236	656	HN00052	ACCTGTGGACCTGGTAGACG	CCACTACCACACCAGGCTCT
31J7-sp6	34H10	932147	206	intergenic	TCCAAGTGAATCCCCAAGAG	ATCAGGCACGGTCTTCGATTA
3O10	gap	1005448	320	intergenic	ACCCCAGGTTTCGGAAATAA	CAGGGTGTGACGACGATAAA
GCP/Bm5536	gap	1124127	557	BM05536	CACGTCAATGAGATGGCAGT	AACTATGCACCCCTGAAGCA
NudC/Bm5586	23N8	1351299	671	HN00121	TATTCAATTTTCTCGCAAGG	CCCTCACTGATACTCCAGAA
Srp68/Bm5593	1K7	1946672	854	BM05593	CGTCGTGTCACAGTGCGCCC	TACTTGTCACTCTTGCCCCA
Unlinked markers						
Bm18W	unlinked	LG18, BmCh23	1274	BM11038	TAGGGTCGTAATTCTGGGTC	AAACAATATGACTGCCACCA
LAM	unlinked	LG17, BmCh13	863	BM00910	TCCAGAATGCTATGCTTGTG	TTAATTCAGATGTAAGCTCT
Sumo	unlinked	(not mapped)	678	BM02755	CCAAATCCGCTTATGG	GAAGAAAAACATGTTATTAT
TL	unlinked	LG09, BmCh07	660	BM10185	GATGCCACGTCCGTTAGAGA	CTATGAGCTTGTTGAATACC
VAS	unlinked	LG13, BmCh22	639	BM00231	ATCACAAGACTTCTCCGTTT	TTTTCTTCTTAAGTTACTGG
AATC	unlinked	LG18, BmCh23	795	BM11029	TGATTTTAAGCTGCACAAGGA	ACTTACAATTTTTCAATCAT
CDP	unlinked	LG12, BmCh08	747	BM05460	AACAAAATGGGAAAAACATC	TCCTTGTATGGGGGATTGAT
CAT	unlinked	LG21, BmCh01	1039	BM00701	TCAAGACTGCGATTCAAACA	TGTCTTCAGTTTGTCCACT
CMD	unlinked	LG19, BmCh12	825	BM10423	CTTTTGTATCAAATTGCATCT	AATCTTTACAAACATCTAG
HCL	unlinked	LG18, BmCh23	706	BM11272	GCCGTAAAAGCAACCAC	AACATATAAATTACACCAAA
Hsp90	unlinked	BmCh27	980	BM04612	AAATGCCAGAGGAAAAAATG	GATAAGGTCTTCACAGTTGT
ATPs	unlinked	LG06, BmCh09	1034	BM12555	GCAGGAAAAGGCCAAGG	TCCATACCCAAGATGCAAT
Cna	unlinked	LG20, BmCh10	1116	BM06850	GTGCCACCTTATTACGAT	TGGTGGCATCCTTTCATTT
TRP_exon1-2	unlinked	LG13, BmCh14	473	BM09272	GAGGACGACGTGATGGAGAT	CCGATTTGGAAGTCCTTGAG
c30739_exon3-4	unlinked	LG13, BmCh14	514	BM09230	CGCATCTAGCCACAGATGAA	GATAGGGGTTCGGATGGTTT
c6511_exon3-4	unlinked	LG13, BmCh14	583	BM09232	TCAATTTGACCAACCACTCG	TAAATCGAACGGCGTACCTC
20L19_Ge03	unlinked	LG17, BmCh13	634	intergenic	AAATCCATGAACTTGGTTTACAA	TGAGAAACCGGTTGACTTGG
20L19_Ge30B	unlinked	LG17, BmCh27	525	BM04620	AACGCTAAACGGGCGGTA	TATCATTTTGTGTATTTTGAGGATTTT

† Estimated position (in kilobases) along the walk taking into account the hypothesised length of the gaps, based on the *H. melpomene HmYb-HmSb* walk. Unlinked markers are assigned to a putative linkage group (LG) based on their chromosome location in the *Bombyx mori* genome (BmCh) and known linkage group homologies.

‡ *Bombyx mori* orthologs of unlinked genes are given. BM prefix stands for the BGIBMGA0 prefix in *B. mori* annotation (e.g. BM12555 = BGIBMGA012555).

Table S9. NCBI Accession numbers for population sets

Region	Gene Marker	n seq	Accessions
Peru	Acetoacetyl-CoA thiolase (Aact) gene	42	JN174613 - JN174654
Peru	Putative ARP-like (HM00028)	41	JN174802 - JN174842
Peru	Putative ATPbinding protein (Bm5558, HN00023) gene	34	JN173999 - JN174032
Peru	H+ transporting ATP synthase beta subunit (ATPs) gene	38	JN175124 - JN175161
Peru	8 wheeler gene (Bm18W)	37	JN174182 - JN174218
Peru	Catalase (CAT) gene	35	JN174074 - JN174108
Peru	Cell division protein (CDP/FtsJ) gene	40	JN174655 - JN174694
Peru	Cytosolic malate dehydrogenase (CMD/ MDH) gene	25	JN174109 - JN174133
Peru	Calcineurin A (cna) gene	41	JN174033 - JN174073
Peru	Putative DNA excision repair protein ERCC-6	51	JN173948 - JN173998
Peru	Forkhead protein (Fox, FH) gene	53	JN174295 - JN174347
Peru	Putative Guanylate (GCP) cyclase	40	JN174843 - JN174882
Peru	Hairy cell leukemia (HCL) gene	36	JN174348 - JN174383
Peru	Heat shock protein (Hsp90) gene	35	JN174384 - JN174418
Peru	Hypothetical protein (HM00021) gene	96	JN173852 - JN173947
Peru	Putative Invertase (BmSuc) gene	62	JN174883 - JN174944
Peru	Laminin (LM) gene	29	JN174773 - JN174801
Peru	Leucine-rich repeat protein (LRR) gene	95	JN174945 - JN175039
Peru	Putative Shuttle craft (NFX1)	46	JN175078 - JN175123
Peru	Putative Nuclear distribution protein NUDC	41	JN174695 - JN174735
Peru	26S proteasome non-ATPase subunit 4 (Pros54/ Psmd4) gene	40	JN174219 - JN174258
Peru	Putative U3 small nucleolar RNA-interacting protein 2 (RNU)	39	JN174419 - JN174457
Peru	Helicase (RecQ) gene	45	JN173798 - JN173851
Peru	Putative signal recognition particle (Srp68) gene	37	JN174736 - JN174772
Peru	SUMO-1 activating enzyme (SAE1) gene	34	JN174458 - JN174491
Peru	Trachealess (TL/ Trh) gene	41	JN174532 - JN174572
Peru	Trehalase 1a (treh-1a) gene	40	JN174492 - JN174531
Peru	Putative Penguin (XTP5)	40	JN174573 - JN174612
Peru	ATP synthase 21 kDa proteolipid subunit (VAS) gene	36	JN174259 - JN174294
FG	Putative DNA excision repair protein ERCC-6	38	JN175040 - JN175077
FG	Leucine-rich repeat protein (LRR) gene	14	JN174134 - JN174147
FG	Putative U3 small nucleolar RNA-interacting protein 2 (RNU)	34	JN174148 - JN174181

*FG=French Guiana

Supplementary References

1 Brudno, M. *et al.* Glocal Alignment: Finding Rearrangements During Alignment. *Bioinformatics* **19S1**, i62, (2003).

2 Frazer, K. A., Pachter, L., Poliakov, A., Rubin, E. M. & Dubchak, I. VISTA: computational tools for comparative genomics. *Nucl. Acids Res.* **32**, W273-W279, (2004).

3 Mayor, C. *et al.* VISTA: Visualizing Global DNA Sequence Alignments of Arbitrary Length. *Bioinformatics* **16**, 1046, (2000).

4 Forster, P., Torroni, A., Renfrew, C. & Rohl, A. Phylogenetic star contraction applied to Asian and Papuan mtDNA evolution. *Mol. Biol. Evol.* **18**, 1864-1881, (2001).

5 Salazar, C., Jiggins, C. D., Taylor, J. E., Kronforst, M. R. & Linares, M. Gene flow and the genealogical history of Heliconius heurippa. *BMC Evol. Biol.* **8**, (2008).

6 Brown, K. S. An illustrated key to the silvaniform *Heliconius* (Lepidoptera: Nymphalidae) with descriptions of new subspecies. *Trans. Amer. Entom. Soc.* **102**, 373-484, (1976).

7 Librado, P. & Rozas, J. DnaSP v5: a software for comprehensive analysis of DNA polymorphism data. *Bioinformatics* **25**, 1451-1452, (2009).

8 Joron, M., Wynne, I. R., Lamas, G. & Mallet, J. Variable selection and the coexistence of multiple mimetic forms of the butterfly *Heliconius numata*. *Evol. Ecol.* **13**, 721-754, (1999).

9 Joron, M. *et al.* A conserved supergene locus controls colour pattern diversity in *Heliconius* butterflies. *PLoS Biol.* **4**, e303, (2006).